

## RAW SEQUENCE LISTING

DATE: 04/30/2001

PATENT APPLICATION: US/09/668,021

TIME: 14:17:32

Input Set : N:\Crf3\RULE60\09668021.txt

Output Set: N:\CRF3\04302001\I668021.raw

4 <110> APPLICANT: Brunkow, Mary E.  
5 Galas, David J.  
6 Kovacevich, Brian  
7 Mulligan, John T.  
8 Paeper, Bryan W.  
9 Van Ness, Jeffrey  
10 Winkler, David G.  
13 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING  
14 BONE MINERALIZATION  
16 <130> FILE REFERENCE: 240083.508  
18 <140> CURRENT APPLICATION NUMBER: 09/668,021  
19 <141> CURRENT FILING DATE: 2000-09-21  
22 <150> PRIOR APPLICATION NUMBER: 09/449,218  
23 <151> PRIOR FILING DATE: 1999-11-24  
25 <160> NUMBER OF SEQ ID NOS: 41  
27 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
29 <210> SEQ ID NO: 1  
30 <211> LENGTH: 2301  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Homo sapien  
34 <400> SEQUENCE: 1

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| 36 | tggeccctgtg | tctcgtctgc | ctgctggtac | acacagcctt | ccgtgtagtg | gagggccagg | 120  |
| 37 | ggtggcaggc  | gttcaagaat | gatgccacgg | aaatcatccc | cgagctcgga | gagtaccccg | 180  |
| 38 | agcctccacc  | ggagctggag | aacaacaaga | ccatgaaccg | ggcggagaac | ggagggcggc | 240  |
| 39 | ctccccacca  | cccttttgag | accaaagacg | tgtccgagta | cagctgccgc | gagctgcaat | 300  |
| 40 | tcaccgccta  | cgtgaccgat | gggcggtgcc | gcagcgccaa | gccggtcacc | gagctggtgt | 360  |
| 41 | gtcccgccca  | gtgcggcccg | gcgcgcctgc | tgcccaacgc | catcggccgc | ggcaagtggg | 420  |
| 42 | ggcgacctag  | tgggcccgac | ttccgctgca | tccccgaccg | ctaccgcgcg | cagcgcgtgc | 480  |
| 43 | agctgctgtg  | tcccgggtgt | gaggcgccgc | gcgcgcgcaa | ggtgcgcctg | gtggcctcgt | 540  |
| 44 | gcaagtgcaa  | gcgcctcacc | cgcttccaca | accagtcgga | gctcaaggac | ttcgggaccg | 600  |
| 45 | aggccgctcg  | gccgcagaag | ggccggaagc | cgccggcccc | cgcccgagac | gccaaagcca | 660  |
| 46 | accaggccga  | gctggagaac | gcctactaga | gcccgccgcg | gcccctcccc | accggcgggc | 720  |
| 47 | gccccggccc  | tgaaccgcgc | ccccacattt | ctgtcctctg | cgcgtggttt | gattgtttat | 780  |
| 48 | atttcattgt  | aaatgcctgc | aaccagggc  | agggggctga | gaccttccag | gccctgagga | 840  |
| 49 | atccccggcg  | ccggcaaggc | ccccctcagc | ccgccagctg | aggggtccca | cggggcaggg | 900  |
| 50 | gaggggaattg | agagtcacag | acactgagcc | acgcagcccc | gcctctgggg | ccgcctacct | 960  |
| 51 | ttgctggtcc  | cacttcagag | gaggcagaaa | tggaagcatt | ttcaccgccc | tggggtttta | 1020 |
| 52 | agggagcggg  | gtgggagtgg | gaaagtccag | ggactgggta | agaaagttag | ataagattcc | 1080 |
| 53 | cccttgccacc | tcgctgcccc | tcagaaagcc | tgaggcgtgc | ccagagcaca | agactggggg | 1140 |
| 54 | caactgtaga  | tgtggtttct | agtctctggt | ctgccactaa | cttgctgtgt | aaccttgaa  | 1200 |
| 55 | tacacaattc  | tccttcggga | cctcaatttc | cactttgtaa | aatgaggggt | gaggtgggaa | 1260 |
| 56 | taggatctcg  | aggagactat | tggcatatga | ttccaaggac | tccagtgcct | tttgaatggg | 1320 |
| 57 | cagaggtgag  | agagagagag | agaaagagag | agaatgaatg | cagttgcatt | gattcagtg  | 1380 |
| 58 | caaggtcact  | tccagaattc | agagttgtga | tgctctcttc | tgacagccaa | agatgaaaa  | 1440 |
| 59 | caaacagaaa  | aaaaaaagta | aagagtctat | ttatggctga | catatttacg | gctgacaaac | 1500 |
| 60 | tcctggaaga  | agctatgctg | cttcccagcc | tggtctcccc | ggatgtttgg | ctacctccac | 1560 |

ENTERED

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Input Set : N:\Crif3\RULE60\09668021.txt

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61 ccctccatct caaagaaata acatcatcca ttggggtaga aaaggagagg gtccgagggt 1620
62 ggtgggaggg atagaaatca catccgcccc aacttcccaa agagcagcat ccctcccccg 1680
63 acccatagcc atgttttaaa gtcacottcc gaagagaagt gaaaggttca aggacactgg 1740
64 ccttgaggc ccgagggagc agccatcaca aactcacaga ccagcacatc ctttttgaga 1800
65 caccgccttc tgcccaccac tcacggacac atttctgcct agaaaacagc ttcttactgc 1860
66 tcttacatgt gatggcatat cttacactaa aagaatatta ttgggggaaa aactacaagt 1920
67 gctgtacata tgctgagaaa ctgcagagca taatagctgc cacccaaaaa tctttttgaa 1980
68 aatcatttcc agacaacctc ttactttctg tgtagttttt aattgttaaa aaaaaaaagt 2040
69 tttaaacaga agcacatgac atatgaaagc ctgcaggact ggtcgttttt ttggcaattc 2100
70 ttocacgtgg gacttgtcca caagaatgaa agtagtggtt tttaaagagt taagttacat 2160
71 atttattttc tcaacttaagt tatttatgca aaagtttttc ttgtagagaa tgacaatgtt 2220
72 aatattgctt tatgaattaa cagtctgttc ttccagagtc cagagacatt gttaataaag 2280
73 acaatgaatc atgaccgaaa g 2301
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76 <211> LENGTH: 213
77 <212> TYPE: PRT
78 <213> ORGANISM: Homo sapien
80 <400> SEQUENCE: 2
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83 Ala Phe Arg Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp
84 20 25 30
85 Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro
86 35 40 45
87 Glu Leu Glu Asn Asn Lys Thr Met Asn Arg Ala Glu Asn Gly Gly Arg
88 50 55 60
89 Pro Pro His His Pro Phe Glu Thr Lys Asp Val Ser Glu Tyr Ser Cys
90 65 70 75 80
91 Arg Glu Leu His Phe Thr Arg Tyr Val Thr Asp Gly Pro Cys Arg Ser
92 85 90 95
93 Ala Lys Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys Gly Pro Ala
94 100 105 110
95 Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro Ser
96 115 120 125
97 Gly Pro Asp Phe Arg Cys Ile Pro Asp Arg Tyr Arg Ala Gln Arg Val
98 130 135 140
99 Gln Leu Leu Cys Pro Gly Gly Glu Ala Pro Arg Ala Arg Lys Val Arg
100 145 150 155 160
101 Leu Val Ala Ser Cys Lys Cys Lys Arg Leu Thr Arg Phe His Asn Gln
102 165 170 175
103 Ser Glu Leu Lys Asp Phe Gly Thr Glu Ala Ala Arg Pro Gln Lys Gly
104 180 185 190
105 Arg Lys Pro Arg Pro Arg Ala Arg Ser Ala Lys Ala Asn Gln Ala Glu
106 195 200 205
107 Leu Glu Asn Ala Tyr
108 210
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 2301
112 <212> TYPE: DNA

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115 <400> SEQUENCE: 3
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117 tggccctgtg tctcgtctgc ctgctgttac acacagcctt ccgtgtagtg gagggctagg 120
118 ggtggcaggc gttcaagaat gatgccacgg aaatcatccc cgagctcgga gactaccccg 180
119 agcctccacc ggagctggag aacaacaaga ccatgaaccg ggccggagaac ggagggcggc 240
120 ctccccacca cccctttgag accaaagacg tgtccgagta cagctgccgc gagctgcaact 300
121 tcacccgcta cgtgaccgat gggccgtgcc gcagcgccaa gccggtcacc gagctggtgt 360
122 gctccggcca gtgcggcccc gcgcgcctgc tgcaccaacgc catcgccgcg ggcaagtgg 420
123 ggcgacctag tgggcccgcac ttccgctgca tccccgaccg ctaccgcgcg cagcgcgtgc 480
124 agctgctgtg tcccgggtgtt gaggcgccgc gcgcgcgcaa ggtgcgcctg gtggcctcgt 540
125 caaagtgcga gcgcctcacc cgcttcacac accagtcgga gctcaaggac ttcgggaccg 600
126 aggcgcctcg gccgcagaag ggccggaagc cgccgccccg cgcgggagc gccaaagcca 660
127 accaggccga gctggagaac gcctactaga gccgcgccgc gccctcccc accggcgggc 720
128 gccccggccc tgaacccgcg cccacattt ctgtcctctg cgcgtggttt gattgtttat 780
129 atttcattgt aaatgcctgc aaccagggc agggggctga gaccttcag gccctgagga 840
130 atcccggcg ccggcaaggc cccctcagc ccgccagctg aggggtccca cggggcaggg 900
131 gaggggaattg agagtccag acactgagcc acgcagcccc gcctctgggg ccgcctacct 960
132 ttgctgttcc cacttcagag gaggcagaaa tgaagcatt ttcaccgcc tggggtttta 1020
133 agggagcggg gtgggagtg gaaagtccag ggactggtta agaaagtgg ataagattcc 1080
134 ccttgccacc tcgtgcacca tcagaaagcc tgaggcgtgc ccagagcaca agactggggg 1140
135 caactgtaga tctggtttct agtctgtgct ctgccactaa cttgctgtgt aacctgaac 1200
136 tacacaattc tcttcggga cctcaatttc cactttgtaa aatgagggg gaggtgggaa 1260
137 taggatctcg aggagactat tggcatatga ttccaaggac tccagtgcct tttgaatggg 1320
138 cagaggtgag agagagagag agaaagagag agaataatg cagttgcatt gattcagtgc 1380
139 caaggtaact tcagaaattc agagtgtgta tgcctctctc tgacagccaa agatgaaaaa 1440
140 caaacagaaa aaaaaagta aagagtctat ttatggctga catatttac gctgacaaac 1500
141 tcttgaaga agctatgctg cttccagcc tggcttcccc ggatgtttg ctacctcac 1560
142 cctccatct caaagaaata acatcatcca ttggggtaga aaaggagagg gtccgagggt 1620
143 ggtgggaggg atagaaatca catccgcccc aacttcccaa agagcagcat cctcccccg 1680
144 acccatagcc atgttttaaa gtcaccttcc gaagagaagt gaaaggttca aggacactgg 1740
145 ccttgccagg ccgaggggagc agccatcaca aactcacaga ccagcacatc ccttttgaga 1800
146 caccgccttc tgcccaccac tcacggacac atttctgcct agaaaacagc ttcttactgc 1860
147 tcttacatgt gatggcatat cttacactaa aagaatatta ttgggggaaa aactacaagt 1920
148 gctgtacata tgcagagaaa ctgcagagca taatagctgc caccacaaaa tctttttgaa 1980
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151 ttccacgtgg gacttgtcca caagaatgaa agtagtggtt tttaaagagt taagttacat 2160
152 atttattttc tcacttaagt tatttatgca aaagttttc ttgtagagaa tgacaatggt 2220
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154 acaatgaatc atgaccgaaa g 2301
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157 <211> LENGTH: 23
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapien
161 <400> SEQUENCE: 4
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163 1 5 10 15
164 Ala Phe Arg Val Val Glu Gly

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168 <211> LENGTH: 2301
169 <212> TYPE: DNA
170 <213> ORGANISM: Homo sapien
172 <400> SEQUENCE: 5
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175 ggtggcaggc gttcaagaat gatgccacgg aaatcatccg cgagctcgga gagtaccccg      180
176 agcctccacc ggagctggag aacaacaaga ccatgaaccg ggcggagaac ggagggcggc      240
177 ctccccacca cccctttgag accaaagacg tgtccgagta cagctgccgc gagctgcact      300
178 tcaccgcgta cgtgaccgat gggccgtgcc gcagcgccaa gccggtcacc gagctggtgt      360
179 gctccgcgca gtgcggcccg gcgcgcctgc tgcccaacgc catcgccgcg gccaagtgtg      420
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181 gactgtgtg tcccggtggt gaggcgcgcg gcgcgcgcaa ggtgcgcctg gtggcctcgt      540
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183 aggcgcgtcg gccgcagaag ggccggaagc cgcggccccc cgcccgagc gccaaagcca      660
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186 atttcattgt aaatgcctgc aaccagggc agggggctga gaccttcag gccctgagga      840
187 atcccgggcg ccggcaaggc cccctcagc ccgccagctg aggggtccca cggggcaggg      900
188 gagggaaattg agagtcacag acactgagcc acgcagcccc gcctctgggg ccgcctacct      960
189 ttgctggtcc cacttcagag gaggcagaaa tggaaagcatt ttcaccgccc tggggtttta      1020
190 agggagcggt gtgggagtgg gaaagtccag ggactggtta agaaagtgg ataagattcc      1080
191 cccttgacc tcgtgcccac tcagaaagcc tgaggcgtgc ccagagcaca agactggggg      1140
192 caactgtaga tgtggtttct agtcctggt ctgccactaa cttgctgtgt aacctgaac      1200
193 tacacaattc tccttcggga cctcaatttc cactttgtaa aatgaggggt gaggtgggaa      1260
194 taggatctcg aggagactat tggcatatga ttccaaggac tccagtgcct tttgaatggg      1320
195 cagaggtgag agagagagag agaaagagag agaatgaatg cagttgcatt gattcagtgc      1380
196 caaggtcact tccagaattc agagttgtga tgctctcttc tgacagccaa agatgaaaaa      1440
197 caaacagaaa aaaaaaagta aagagtctat ttatggctga catatttacg gctgacaaac      1500
198 tcctggaaga agctatgctg cttcccagcc tggcttcccc ggatgttttg ctacctccac      1560
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201 acccatagcc atgttttaaa gtcaccttcc gaagagaagt gaaaggttca aggacactgg      1740
202 ccttgaggc ccgagggagc agccatcaca aactcacaga ccagcacatc ccttttgaga      1800
203 caccgccttc tgcccaccac tcacggacac atttctgcct agaaaacagc ttcttactgc      1860
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205 gctgtacata tgctgagaaa ctgcagagca taatagctgc cacccaaaaa tctttttgaa      1980
206 aatcatttcc agacaacctc ttactttctg tgtagttttt aattgttaaa aaaaaaaagt      2040
207 tttaaacaga agcacatgac atatgaaaag ctgcaggact ggtcgttttt ttggcaattc      2100
208 ttccacgtgg gacttgtcca caagaatgaa agtagtggtt tttaaagagt taagttacat      2160
209 atttattttc tcacttaagt tatttatgca aaagtttttc ttgtagagaa tgacaatgtt      2220
210 aatattgctt tatgaattaa cagtctgttc ttccagagtc cagagacatt gttaataaag      2280
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213 <210> SEQ ID NO: 6
214 <211> LENGTH: 213
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapien

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218 &lt;400&gt; SEQUENCE: 6

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221 Ala Phe Arg Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp
222       20      25      30
223 Ala Thr Glu Ile Ile Arg Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro
224       35      40      45
225 Glu Leu Glu Asn Asn Lys Thr Met Asn Arg Ala Glu Asn Gly Gly Arg
226       50      55      60
227 Pro Pro His His Pro Phe Glu Thr Lys Asp Val Ser Glu Tyr Ser Cys
228       65      70      75      80
229 Arg Glu Leu His Phe Thr Arg Tyr Val Thr Asp Gly Pro Cys Arg Ser
230       85      90      95
231 Ala Lys Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys Gly Pro Ala
232      100     105     110
233 Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro Ser
234      115     120     125
235 Gly Pro Asp Phe Arg Cys Ile Pro Asp Arg Tyr Arg Ala Gln Arg Val
236      130     135     140
237 Gln Leu Leu Cys Pro Gly Glu Ala Pro Arg Ala Arg Lys Val Arg
238      145     150     155     160
239 Leu Val Ala Ser Cys Lys Cys Lys Arg Leu Thr Arg Phe His Asn Gln
240      165     170     175
241 Ser Glu Leu Lys Asp Phe Gly Thr Glu Ala Ala Arg Pro Gln Lys Gly
242      180     185     190
243 Arg Lys Pro Arg Pro Arg Ala Arg Ser Ala Lys Ala Asn Gln Ala Glu
244      195     200     205
245 Leu Glu Asn Ala Tyr
246      210

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248 &lt;210&gt; SEQ ID NO: 7

249 &lt;211&gt; LENGTH: 2301

250 &lt;212&gt; TYPE: DNA

251 &lt;213&gt; ORGANISM: Homo sapien

253 &lt;400&gt; SEQUENCE: 7

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255 tggccctgtg tctcgtctgc ctgctgtgtac acacagcctt ccgtgtagtg gagggccagg      120
256 ggtggcaggc gttcaagaat gatgccacgg aaatcatccg cgagctcgga gactaccccg      180
257 agcctccacc ggagctggag aacaacaaga ccatgaaccg ggcggagaac ggagggcggc      240
258 ctccccacca cccctttgag accaaagacg tgtccgagta cagctgccgc gagctgcact      300
259 tcaccgcgta cgtgaccgat gggccgtgcc gcagcgccaa gccggtcacc gagctggtgt      360
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263 gcaagtgcaa gcgcctcacc cgcttcacca accagtcgga gctcaaggac ttcgggaccg      600
264 aggcgcgtcg gcgcgagaag ggccggaagc cgccggcccg cgcccgagc gccaaagcca      660
265 accaggccga gctggagaac gcctactaga gcccgccgcg gccctcccc accggcgggc      720
266 gccccggccc tgaaccgcgc ccccacattt ctgtcctctg cgcgtgggtt gattgtttat      780
267 atttcattgt aaatgcctgc aaccagggc agggggctga gaccttcag gccctgagga      840
268 atcccgggcg ccggcaaggc ccccctcagc ccgccagctg aggggtccca cggggcaggg      900

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Input Set : N:\Crf3\RULE60\09668021.txt

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L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17

## STATISTICS SUMMARY

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Input Set : N:\Crif3\RULE60\09668021.txt

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Application Serial Number: US/09/668,021

Alpha or Numeric: Numeric

Application Class:

Application File Date: 09-21-2000

Art Unit:

Software Application: FastSeq

Total Number of Sequences: 41

Total Nucleotides: 57700

Total Amino Acids: 1475

Number of Errors: 0

Number of Warnings: 1

Number of Corrections: 0

## MESSAGE SUMMARY

341 W: 1 ((46) "n" or "Xaa" used)